IN THE SPECIFICATION

On page 1, second line, amend as follows:

Attorney Docket No. ~~18002-000210~~107-206-C-D

Please amend the Specification as follows:

On page 6, line 31, amend the paragraph as follows:

D1

Fig. 5 shows the alignment of the amino acid sequences of Repro-PC-1.0 (SEQ ID NO:2) and rat synaptotagmin 4 ("SYT4") (SEQ ID NO:5).

On page 7, line 1, amend the paragraph as follows:

D2

Fig. 6 shows the alignment of the internal repeats of PKC-C2 (SEQ ID NO:6), Repro-PC-1.0 "B" repeat (SEQ ID NO:7), synaptotagmin "B" repeat (SEQ ID NO:8), synaptotagmin "A" repeat (SEQ ID NO:9) and Repro-PC-1.0 "A" repeat (SEQ ID NO:10).

On page 40, amend the paragraph beginning on line 6 as follows:

D3

HLA-A1 binding motif includes a first conserved residue of T, S or M, a second

conserved residue of D or E, and a third conserved residue of Y. Other second conserved residues are A, S or T. The first and second conserved residues are adjacent and are preferably separated from the third conserved residue by 6 to 7 residues (SEQ ID NOS:11 and 12). A second motif consists of a first conserved residue of E or D and a second conserved residue of Y where the first and second conserved residues are separated by 5 to 6 residues (SEQ ID NOS:13 and 14). The HLA-A3.2 binding motif includes a first conserved residue of L, M, I, V, S, A, T and F at position 2 and a second conserved residue of K, R or Y at the C-terminal end. Other first conserved residues are C, G or D and alternatively E. Other second conserved residues are H or F. The first and second conserved residues are preferably separated by 6 to 7 residues (SEQ ID NOS:15 and 16). The HLA-A11 binding motif includes a first conserved residue of T or V at position 2 and a C-terminal conserved residue of K. The first and second conserved residues are preferably separated by 6 to 7 residues (SEQ ID NOS:17 and 18). The HLA-A24.1 binding motif includes a first conserved residue of Y, F or W at position 2 and a C terminal conserved residue of F, I, W, M or L. The first and second conserved residues are preferably separated by 6 to 7 residues (SEQ ID NOS:19 and 20).

On page 41, line 31, amend the paragraph as follows:

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                    |--|  |---|
9       eefdeiptvvgifsafglvftvslfawiccq        (SEQ ID NO:21)
                19 22 25  29
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On page 42, line 3, amend as follows:

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                           |--|
                   |--|         |---|
42   ssksnktppykfvhvlkgvdiypenlnskkkfga      (SEQ ID NO:22)
                   52 55     61   65
                      55 58
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On page 42, line 8, amend as follows:

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                     |---|
114  spsdlenatpklflegekesvspes               (SEQ ID NO:23)
                     124 128
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On page 42, line 13, amend as follows:

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                       |--|
                  |--|         |--|          |---|              |--|
199  lpekkhkvktrvlrkctldpafdetftfygipytqiqelalhftilsfdrfsrddiigevl
                  209          221           235 239            252
                       213
     (SEQ ID NO:24)
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On page 42, line 18, amend as follows:

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                   |---| |--|            |---|
259  iplsgielsegkmlmnreiikrnvrkssgrgellislcyqsttntl      (SEQ ID NO:25)
                   270 274  279          290 294
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On page 42, line 22, amend as follows:

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                   |--|     |---|
376  vldsergsrnevigqlvlgaaaegtggehwkei       (SEQ ID NO:26)
                   386      394 398
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On page 50, line 26 to page 51, line 2, amend the paragraph as follows:

Figure 5 shows the alignment of the amino acid sequences for Repro-PC-1.0 and rat synaptotagmin IV. Repro-PC-1.0 shows 90% overall identity with rat synaptotagmin IV. Like theother synaptotagmin isoforms, Repro-PC-1.0 was most similar to these sequences in the PKC C2 repeat C-terminal region (91% identity). The two internal

repeats of Repro-PC-1.0 are approximately as homologous to each other (34% identity) as to the corresponding region of PKC (identity between 35% and 43# depending on the isoform). As in the other forms of synaptotagin, the amino acid residues that are identical between the two internal repeats of Repro-PC-1.0 are also conserved between Repro-PC-1.0 and PKC, revealing a core consensus sequence of ~~SDPYV/IK~~SDPY(V/I)K (SEQ ID NO:27) followed by a stretch of basic residues (Figure 6).

Please insert the accompanying paper copy of the Sequence Listing, consisting of 19 pages, at the end of the application. Cancel the present "SEQUENCE LISTING, pages 63 through 69, and cancel the page numbers of the Claims and Abstract and renumber accordingly, 63 to 88.